

SOX3MRPVRENSSGARSPRVPADLARSILISLPFPDLSLAHRPPSSAPTESQGLFTVAAPAPGAPSPATLAHLIPAPAMYSLLETETELKNPVGT	90
SOX1	MYSMMETDLHSGGGAQAPTNLSGPAGAGGGGGGGGGGGGAKANQDRVKRPNNARWVWNSRGORRRKVAQENPKMHNSESKRLGAENKVMSEALEKRPRIIDE	103
SOX2	MY-NMME TELKPPGPQOTS-----GCGGCNSTAAAGGNQKNSPDRVKRPNNARWVWNSRGORRRKVAQENPKMHNSESKRLGAENKVMSEALEKRPRIIDE	93
SOX3	PTQAACTGGPAAAGGAGKSSANAAGGANGGGSSGGASGGGG--TDQDRVKRPNNARWVWNSRGORRRKVAQENPKMHNSESKRLGADWKLLTDAEKRPRIIDE	191
SOX21MSKPVDRVKRPNNARWVWNSRAQORRRKVAQENPKMHNSESKRLGAENKVMSEALEKRPRIIDE	60
SOX1	AKTRPALHMKHEHPDVGVRRRKTKTLKKDKVSLA-----GGTAAAGAGGGGAAMGVGVGVGA-APVQRLESPPGGAAGGAYAHVNGWANGAMPGAVAAAA	200
SOX2	AKTRPALHMKHEHPDVGVRRRKTKTLKKDKVSLA-----GGTAAAGAGGGGAAMGVGVGVGA-APVQRLESPPGGAAGGAYAHVNGWANGAMPGAVAAAA	171
SOX3	AKTRPALHMKHEHPDVGVRRRKTKTLKKDKVSLA-----GGTAAAGAGGGGAAMGVGVGVGA-APVQRLESPPGGAAGGAYAHVNGWANGAMPGAVAAAA	272
SOX21	AKTRPALHMKHEHPDVGVRRRKTKTLKKDKVSLA-----GGTAAAGAGGGGAAMGVGVGVGA-APVQRLESPPGGAAGGAYAHVNGWANGAMPGAVAAAA	162
SOX1	AAAAAQEAQLAYGQHPGAGGAHPHRTPAHPHPHHAH-PHNPQPMHRYONGALQSPISN--SQGMSAAPS-----GYGGLPYGAAAAAAAHONSAAVA	295
SOX2	---SMMQD-QLGVQHPGL-----NAHGAQMQPMHRYOVSAQNSMTS--SQTYMNGSPT-----YSMSYSQQGTPG	234
SOX3	---SLVQE-QLGVQHPGL-----NAHGAQMQPMHRYOVSAQNSMTS--SQTYMNGSPT-----YSMSYSQQGTPG	352
SOX21	AAAA-----GSHTHSHPSGPNPGYMITPCNSAWPSGLQPPA---YILLP-GMGKPOLDEYPAAYAAAL	214
SOX1	AAAAAASSGALGALGSLVKSEPSGSP-----APAHSRAPCPGDREMTSMYPRAGSGG---DPAAATAAAQSRHSLPQHYQGA---GAGVNGVPLTHI	387
SOX2	-----MALGSMGSLVKSEASSPSPVVTSSSHSRAPCOAGDRDMISMYLP-CAEVP--EPAA-----PSRLHMS-QHYQSGVPVGTAINGLPLSHM	317
SOX3	AAAAAAMSLGPMGSLVKSEPSGSP-----AIASHSORAC-LGDRDMISMYLP-CAEVP--EPAA-----PSRLHMS-QHYQSGVPVGTAINGLPLSHM	443
SOX21	AAAA-----GSHTHSHPSGPNPGYMITPCNSAWPSGLQPPA---YILLP-GMGKPOLDEYPAAYAAAL	276

Fig. 1